



## SEQUENCE LISTING

<110> Lee, Bruce Andrew  
Flores, Becky Mar  
Valkirs, Gunars Edwin  
Biosite Diagnostics, Inc.

<120> Assays for Detection of Bacillus Anthracis

<130> 014907-003310US

<140> US 09/754,947

<141> 2001-01-04

<150> US 60/174,901

<151> 2000-01-06

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 785

<212> PRT

<213> Bacillus anthracis

<220>

<223> surface array protein (SAP)

<400> 1

Ala Gly Lys Thr Phe Pro Asp Val Pro Ala Asp His Trp Gly Ile Asp  
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Ser Ile Asn Tyr Leu Val Glu Lys Gly Ala Val Lys Gly Asn Asp Lys  
20 25 30

Gly Met Phe Glu Pro Gly Lys Glu Leu Thr Arg Ala Glu Ala Ala Thr  
35 40 45

Met Met Ala Gln Ile Leu Asn Leu Pro Ile Asp Lys Asp Ala Lys Pro  
50 55 60

Ser Phe Ala Asp Ser Gln Gly Gln Trp Tyr Thr Pro Phe Ile Ala Ala  
65 70 75 80

Val Glu Lys Ala Gly Val Ile Lys Gly Thr Gly Asn Gly Phe Glu Pro  
85 90 95

Asn Gly Lys Ile Asp Arg Val Ser Met Ala Ser Leu Leu Val Glu Ala  
100 105 110

Tyr Lys Leu Asp Thr Lys Val Asn Gly Thr Pro Ala Thr Lys Phe Lys  
115 120 125

Asp Leu Glu Thr Leu Asn Trp Gly Lys Glu Lys Ala Asn Ile Leu Val  
130 135 140

Glu Leu Gly Ile Ser Val Gly Thr Gly Asp Gln Trp Glu Pro Lys Lys  
145 150 155 160

Thr Val Thr Lys Ala Glu Ala Ala Gln Phe Ile Ala Lys Thr Asp Lys  
 165 170 175  
 Gln Phe Gly Thr Glu Ala Ala Lys Val Glu Ser Ala Lys Ala Val Thr  
 180 185 190  
 Thr Gln Lys Val Glu Val Lys Phe Ser Lys Ala Val Glu Lys Leu Thr  
 195 200 205  
 Lys Glu Asp Ile Lys Val Thr Asn Lys Ala Asn Asn Asp Lys Val Leu  
 210 215 220  
 Val Lys Glu Val Thr Leu Ser Glu Asp Lys Arg Ser Ala Thr Val Glu  
 225 230 235 240  
 Leu Tyr Ser Asn Leu Ala Ala Lys Gln Thr Tyr Thr Val Asp Val Asn  
 245 250 255  
 Lys Val Gly Lys Thr Glu Val Ala Val Gly Ser Leu Glu Ala Lys Thr  
 260 265 270  
 Ile Glu Met Ala Asp Gln Thr Val Val Ala Asp Glu Pro Thr Ala Leu  
 275 280 285  
 Gln Phe Thr Val Lys Asp Glu Asn Gly Thr Glu Val Val Ser Pro Glu  
 290 295 300  
 Gly Ile Glu Phe Val Thr Pro Ala Ala Glu Lys Ile Asn Ala Lys Gly  
 305 310 315 320  
 Glu Ile Thr Leu Ala Lys Gly Thr Ser Thr Thr Val Lys Ala Val Tyr  
 325 330 335  
 Lys Lys Asp Gly Lys Val Val Ala Glu Ser Lys Glu Val Lys Val Ser  
 340 345 350  
 Ala Glu Gly Ala Ala Val Ala Ser Ile Ser Asn Trp Thr Val Ala Glu  
 355 360 365  
 Gln Asn Lys Ala Asp Phe Thr Ser Lys Asp Phe Lys Gln Asn Asn Lys  
 370 375 380  
 Val Tyr Glu Gly Asp Asn Ala Tyr Val Gln Val Glu Leu Lys Asp Gln  
 385 390 395 400  
 Phe Asn Ala Val Thr Thr Gly Lys Val Glu Tyr Glu Ser Leu Asn Thr  
 405 410 415  
 Glu Val Ala Val Val Asp Lys Ala Thr Gly Lys Val Thr Val Leu Ser  
 420 425 430  
 Ala Gly Lys Ala Pro Val Lys Val Thr Val Lys Asp Ser Lys Gly Lys  
 435 440 445

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Ala Leu Val Ser His Thr Val Glu Ile Glu Ala Phe Ala Gln Lys Ala  
 450 455 460  
 Met Lys Asp Ile Lys Leu Glu Lys Thr Asn Val Ala Leu Ser Thr Lys  
 465 470 475 480

Asp Val Thr Asp Leu Lys Val Lys Ala Pro Val Leu Asp Gln Tyr Gly  
 485 490 495  
 Lys Glu Phe Thr Ala Pro Val Thr Val Lys Val Leu Asp Lys Asp Gly  
 500 505 510  
 Lys Glu Leu Lys Glu Gln Lys Leu Glu Ala Lys Tyr Val Asn Arg Glu  
 515 520 525  
 Leu Val Leu Asn Ala Ala Gly Gln Glu Ala Gly Asn Tyr Thr Val Val  
 530 535 540  
 Leu Thr Ala Lys Ser Gly Glu Lys Glu Ala Lys Ala Thr Leu Ala Leu  
 545 550 555 560  
 Glu Leu Lys Ala Pro Gly Ala Phe Ser Lys Phe Glu Val Arg Gly Leu  
 565 570 575  
 Asp Thr Glu Leu Asp Lys Tyr Val Thr Glu Glu Asn Gln Lys Asn Ala  
 580 585 590  
 Met Thr Val Ser Val Leu Pro Val Asp Ala Asn Gly Leu Val Leu Lys  
 595 600 605  
 Gly Ala Glu Ala Ala Glu Leu Lys Val Thr Thr Thr Asn Lys Glu Gly  
 610 615 620  
 Lys Glu Val Asp Ala Thr Asp Ala Gln Val Thr Val Gln Asn Asn Ser  
 625 630 635 640  
 Val Ile Thr Val Gly Gln Gly Ala Lys Ala Gly Glu Thr Tyr Lys Val  
 645 650 655  
 Thr Val Val Leu Asp Gly Lys Leu Ile Thr Thr His Ser Phe Lys Val  
 660 665 670  
 Val Asp Thr Ala Pro Thr Ala Lys Gly Leu Ala Val Glu Phe Thr Ser  
 675 680 685  
 Thr Ser Leu Lys Glu Val Ala Pro Asn Ala Asp Leu Lys Ala Ala Leu  
 690 695 700  
 Leu Asn Ile Leu Ser Val Asp Gly Val Pro Ala Thr Thr Ala Lys Ala  
 705 710 715 720  
 Thr Ala Ser Asn Val Glu Phe Val Ser Ala Asp Thr Asn Val Val Ala  
 725 730 735  
 Glu Asn Gly Thr Val Gly Ala Lys Gly Ala Thr Ser Ile Tyr Val Lys  
 740 745 750  
 Asn Leu Thr Val Val Lys Asp Gly Lys Glu Gln Lys Val Glu Phe Asp  
 755 760 765  


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 Lys Ala Val Gln Val Ala Val Ser Ile Lys Glu Ala Lys Pro Ala Thr  
 770 775 780  
 Lys  
 785

<210> 2  
 <211> 2370  
 <212> DNA  
 <213> *Bacillus anthracis*

<220>  
 <223> surface array protein (SAP)

<400> 2  
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 gaaaaaggcg cagttaaagg taacgacaaa ggaatgttcg agcctggaaa agaattaact 120  
 cgtgcagaag cagctacaat gatggctcaa atcttaaact taccaatcga taaagatgct 180  
 aaaccatctt tcgctgactc tcaaggccaa tgggtacact cattcatcgc agctgtagaa 240  
 aaagctggcg ttattaaagg tacaggaaac ggctttgagc caaacggaaa aatcgaccgc 300  
 gtttctatgg catctcttct tgtagaagct tacaaattag atactaaagt aaacgggtact 360  
 ccagcaacta aattcaaaga tttagaaaca tttaaactggg gtaaagaaaa agctaactc 420  
 ttagttgaat taggaatctc tgttggtact ggtgatcaat gggagcctaa gaaaactgta 480  
 actaaagcag aagctgctca attcattgct aagactgaca agcagttcgg tacagaagca 540  
 gcaaaagttg aatctgcaaa agctgttaca actcaaaaag tagaagttaa attcagcaaa 600  
 gctgttgaaa aattaactaa agaagatctc aaagtaacta acaaagctaa caacgataaa 660  
 gtactagtta aagaggtaac tttatcagaa gataaaaagt ctgctacagt tgaattatat 720  
 agtaacttag cagctaaaca aacttacact gtagatgtaa acaaagttgg taaaacagaa 780  
 gtagctgtag gttctttaga agcaaaaaca atcgaaatgg ctgaccacaa acgtttagct 840  
 gatgagccaa cagcattaca attcacagtt aaagatgaaa acggtactga agttgtttca 900  
 ccagagggtg ttgaatttgt aacgccagct gcagaaaaaa ttaatgcaaa aggtgaaatc 960  
 actttagcaa aaggtacttc aactactgta aaagctgttt ataaaaaaga cggtaaagta 1020  
 gtagctgaaa gtaaagaagt aaaagtttct gctgaagggtg ctgcagtagc ttcaatctct 1080  
 aactggacag ttgcagaaca aaataaagct gactttactt ctaaagattt caaacaaaac 1140  
 aataaagttt acgaaggcga caacgcttac gttcaagtag aattgaaaga tcaatttaac 1200  
 gcagtaacaa ctggaaaagt tgaatatgag tcgttaaaca cagaagttgc ttagtagat 1260  
 aaagctactg gtaaagtaac tgtattatct gcaggaaaag caccagtaaa agtaactgta 1320  
 aaagattcaa aaggtaaagc acttgtttca cacacagttg aaattgaagc tttcgctcaa 1380  
 aaagcaatga aagacattaa attagaaaaa actaacgtag cgctttctac aaaagatgta 1440  
 acagatttaa aagtaaaagc tccagtacta gatcaatacg gtaaagagtt tacagctcct 1500  
 gtaacagtga aagtacttga taaagatggt aaagaattaa aagaacaaaa attagaagct 1560  
 aaatatgtga acagagaatt agttctgaat gcagcaggtc aagaagctgg taattataca 1620  
 gttgtattaa ctgcaaaatc tgggtgaaaa gaagcaaaaag ctacattagc tctagaatta 1680  
 aaagctccag gtgcattctc taaatttgaa gttcgtggtt tagacacaga attagataaa 1740  
 tatgttactg aggaaaacca aaagaatgca atgactgttt cagttcttcc ttagatgca 1800  
 aatggattag tattaaaagg tgcagaagca gctgaactaa aagtaacaac acaaaacaaa 1860  
 gaaggtaaaag aagtagacgc aactgatgca caagttactg tacaaaataa cagtgtatt 1920  
 actgttggtc aaggtgcaaa agctggtgag acttataaag taacagttgt actagatggt 1980  
 aaattaatca caactcattc attcaaagtt gttgatacag caccaactgc taaaggatta 2040  
 gcagtagaat ttacaagcac atctcttaaa gaagtagctc caaatgctga tttaaaagct 2100  
 gcacttttaa atatcttatc tgttgatggt gtacctgcga ctacagcaaa agcaacagct 2160  
 tctaattgtag aatttggttc tgctgacaca aatgtttag ctgaaaatgg tacagttggt 2220  
 gcaaaagggtg caacatctat ctatgtgaaa aacctgacag ttgtaaaaga tggaaaagag 2280  
 caaaaagtag aatttgataa agctgtacaa gttgcagttt ctattaaaga agcaaaacct 2340  
 gcaacaaaac atcaccatca ccatcactaa 2370

<210> 3  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:5' PCR primer

<400> 3  
 tcgctgcccc accagccatg gccgcaggta aaacattccc agac

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<400> 4
gtgataaact accgcattaa agcttatcga tgataagctg tcaattagtg atgggtgatgg 60
tgatgttttg ttgcaggttt tgcttcttt                                     89
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```
<210> 5
<211> 201
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:flexible linker
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<220>
<221> MOD_RES
<222> (1)..(97)
<223> Gly at positions 1-97 may be present or absent
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<220>
<221> MOD_RES
<222> (105)..(201)
<223> Gly at positions 105-201 may be present or absent
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Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
          1                      5                      10                      15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly

20                      25                      30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
35 40 45

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
50                      55                      60

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
65                      70                      75                      80

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly

85    90    95

Gly Gly Gly Gly Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
100 105 110

Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
		115				120					125			

[illegible]

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
145                      150                      155                      160

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
165 170 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
180 185 190

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
195 200

aa<sup>3</sup>.

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